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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=1; day=22; hr=16; min=26; sec=44; ms=514;]

=====

Reviewer Comments:

<210> 56

<211> 17752

<212> DNA

<213> *Phaeodactylum tricornutum*, *Physcomitrella patens*

<210> 71

<211> 17061

<212> DNA

<213> *Phaeodactylum tricornutum*, *Physcomitrella patens*, *Caenorhabditis elegans*

The above <213> responses for sequence id#'s 56 and 71 are both invalid, only one organism response is allowed for this line.

<210> 100

<211> 25

<212> DNA

<213> unknown

<220>

<221> misc_feature

<222> (1)..(25)

<223> ACtrau-5'

<210> 103

<211> 22
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(22)
<223> YES-HIS-5'

Please explain the above <223> responses for sequence id#s 100 and 103.
FYI, please do not use foreign language in U.S. applications. Please
correct the remaining sequences showing similar errors.

Application No: 10552013

Version No: 2.0

Input Set:**Output Set:**

Started: 2009-01-07 16:25:11.916
Finished: 2009-01-07 16:25:23.759
Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 843 ms
Total Warnings: 109
Total Errors: 51
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (28)
W 402	Undefined organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (30)
W 402	Undefined organism found in <213> in SEQ ID (31)
W 402	Undefined organism found in <213> in SEQ ID (32)
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (36)
W 402	Undefined organism found in <213> in SEQ ID (37)
W 213	Artificial or Unknown found in <213> in SEQ ID (52)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (52)
W 213	Artificial or Unknown found in <213> in SEQ ID (53)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (53)
W 213	Artificial or Unknown found in <213> in SEQ ID (54)

Input Set:

Output Set:

Started: 2009-01-07 16:25:11.916
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Total Warnings: 109
Total Errors: 51
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (54)
W 213	Artificial or Unknown found in <213> in SEQ ID (55)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (55)
W 402	Undefined organism found in <213> in SEQ ID (56)
W 402	Undefined organism found in <213> in SEQ ID (57)
W 402	Undefined organism found in <213> in SEQ ID (58)
W 402	Undefined organism found in <213> in SEQ ID (59)
W 213	Artificial or Unknown found in <213> in SEQ ID (60)
W 213	Artificial or Unknown found in <213> in SEQ ID (61)
W 213	Artificial or Unknown found in <213> in SEQ ID (62)
W 213	Artificial or Unknown found in <213> in SEQ ID (63)
W 213	Artificial or Unknown found in <213> in SEQ ID (64)
W 213	Artificial or Unknown found in <213> in SEQ ID (65)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (65)
W 213	Artificial or Unknown found in <213> in SEQ ID (66)
W 213	Artificial or Unknown found in <213> in SEQ ID (67)
W 213	Artificial or Unknown found in <213> in SEQ ID (68)
W 402	Undefined organism found in <213> in SEQ ID (71)
W 402	Undefined organism found in <213> in SEQ ID (72) This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (75)

Input Set:

Output Set:

Started: 2009-01-07 16:25:11.916
Finished: 2009-01-07 16:25:23.759
Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 843 ms
Total Warnings: 109
Total Errors: 51
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (76)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (76)
W 213	Artificial or Unknown found in <213> in SEQ ID (77)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (77)
W 213	Artificial or Unknown found in <213> in SEQ ID (78)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (78)
W 213	Artificial or Unknown found in <213> in SEQ ID (79)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (79)
W 213	Artificial or Unknown found in <213> in SEQ ID (80)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (80)
W 213	Artificial or Unknown found in <213> in SEQ ID (81) This error has occurred more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (81)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (82)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (83)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (84)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (85)

Input Set:

Output Set:

Started: 2009-01-07 16:25:11.916
Finished: 2009-01-07 16:25:23.759
Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 843 ms
Total Warnings: 109
Total Errors: 51
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (86)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (87)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (88)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (89) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Renz, Andreas
Sozer, Nursen
Frentzen, Margit
Bauer, Jorg
Keith, Stobart
Fraser, Thomas
Lazarus, Colin M
Qi, Baoxiu
Abbadie, Amine
Heinz, Ernst

<120> NOVEL PLANT ACYLTRANSFERASES SPECIFIC FOR LONG-CHAINED, MULTIPLY
UNSATURATED FATTY ACIDS

<130> 13478-00002-US

<140> 10552013

<141> 2005-09-30

<150> PCT/EP2004/003224

<151> 2004-03-26

<150> DE103 14 759.4

<151> 2003-03-31

<150> DE103 48 996.7

<151> 2003-10-17

<160> 148

<170> PatentIn version 3.3

<210> 1

<211> 1047

<212> DNA

<213> Thraustochytrium

<220>

<221> CDS

<222> (38)..(952)

<223> LPAAT

<400> 1

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				Met	Ser	Ala	Trp	Thr	Arg								
				1			5										
gcc	aag	acc	gcc	gtg	ggc	ctc	ctg	acg	ctg	ggt	ctt	gct	gct	ggt	ata	gtg	103
Ala	Lys	Thr	Ala	Val	Gly	Leu	Leu	Thr	Leu	Ala	Pro	Ala	Arg	Ile	Val		
10				15			20										
ttc	ctc	gtg	act	gtc	ctg	ggc	acg	tac	ggg	ctc	acg	gtc	gct	gct	gtc	151	
Phe	Leu	Val	Thr	Val	Leu	Gly	Thr	Val	Gly	Thr	Tyr	Gly	Leu	Thr	Val	Ala	Ala
25				30			35										
acg	cga	ctt	ggc	gtc	ccg	aaa	agc	ttc	gtg	ctg	ggc	acg	ccg	ttc		199	

Thr Arg Leu Gly Val Pro Lys Ser Phe Val Leu Gly Leu Thr Arg Cys				
40	45	50		
gtc gcg cga ctc acg ctc tgg ggg ctt ggg ttc tac cac att gag gtc			247	
Val Ala Arg Leu Thr Leu Trp Gly Leu Gly Phe Tyr His Ile Glu Val				
55	60	65	70	
tct tgc gac gcc caa ggc ctt cgg gag tgg cgg cgc gtg att gtc gcg			295	
Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp Pro Arg Val Ile Val Ala				
75	80	85		
aac cac gtc tcc tac ctg gag atc ttg tac ttc atg tcc acc gtg cac			343	
Asn His Val Ser Tyr Leu Glu Ile Leu Tyr Phe Met Ser Thr Val His				
90	95	100		
tgc cgg tct ttc gtc atg aag aac acc tgc ctc cga gtc ccc ctt gtc			391	
Cys Pro Ser Phe Val Met Lys Lys Thr Cys Leu Arg Val Pro Leu Val				
105	110	115		
ggc tac att gcc atg gag ctg ggc ggt gtg att gtg gac cgc gag ggc			439	
Gly Tyr Ile Ala Met Glu Leu Gly Gly Val Ile Val Asp Arg Glu Gly				
120	125	130		
ggc ggt caa aac gca tcc gcg atc att cgc gac cgc gtg cag gag cct			487	
Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg Asp Arg Val Gln Glu Pro				
135	140	145	150	
cct cga gat tcc tcc agc gag aag cac cac ggg cag ccc ctt ctt gtg			535	
Pro Arg Asp Ser Ser Ser Glu Lys His His Ala Gln Pro Leu Val				
155	160	165		
ttc ccc gag ggg acc acc aat gga aac tcc tcc cca ttc aag			583	
Phe Pro Glu Gly Thr Thr Asn Gly Ser Cys Leu Leu Gln Phe Lys				
170	175	180		
acg gga gcc ttt cgt cct ggg gct ccc gtg ctt ccc gtc gtg ctt gag			631	
Thr Gly Ala Phe Arg Pro Gly Ala Pro Val Leu Pro Val Val Leu Glu				
185	190	195		
ttt ccg att gac aaa ggc cgt ggt gac ttt tcc ccc ggg tac gaa tcc			679	
Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe Ser Pro Ala Tyr Glu Ser				
200	205	210		
gtc cac acg cca gct cac ctc ctt cgc atg ctc gca caa tgg agg cac			727	
Val His Thr Pro Ala His Leu Leu Arg Met Leu Ala Gln Trp Arg His				
215	220	225	230	
cgg ctt cgg gtg cgc tat ctt ccc ctg tat gag ccc tct ggg gtc gag			775	
Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr Glu Pro Ser Ala Ala Glu				
235	240	245		
aag gtt gat gca gac ctt tat ggc cgg aac gtg cgc gac gaa atg gcg			823	
Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn Val Arg Asp Glu Met Ala				
250	255	260		
cgc gcg ctc aag gta ccc act gtg gag cag tac tcc cgc gac aag ctc			871	
Arg Ala Leu Lys Val Pro Thr Val Glu Gln Ser Tyr Arg Asp Lys Leu				
265	270	275		
gtc tac cac ggc gat ctc atg ccc cac tac cag aac gcc ggc ccc gga			919	
Val Tyr His Ala Asp Leu Met Pro His Tyr Gln Lys Ala Gly Pro Gly				
280	285	290		
gtc ctc tat ctg tac gtc cga ccc act gac ctc ttg tagactctat gggcggtccca			972	
Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu Leu				
295	300	305		
aaaaaaaaaaaaaa aaaaaaaaaaaaaaa aaaaaaaaaaaaaaa aaaaaaaaaaaaaaa			1032	
aaaaaaaaaaaaaa aaaaaa			1047	

<210> 2

<211> 305

<212> PRT

<213> Thraustochytrium

<400> 2

Met Ser Ala Trp Thr Arg Ala Lys Thr Ala Val Gly Leu Leu Thr Leu
1 5 10 15
Ala Pro Ala Arg Ile Val Phe Leu Val Thr Val Leu Gly Thr Tyr Gly
20 25 30
Leu Thr Val Ala Ala Cys Thr Arg Leu Gly Val Pro Lys Ser Phe Val
35 40 45
Leu Gly Leu Thr Arg Cys Val Ala Arg Leu Thr Leu Trp Gly Leu Gly
50 55 60
Phe Tyr His Ile Glu Val Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp
65 70 75 80
Pro Arg Val Ile Val Ala Asn His Val Ser Tyr Leu Glu Ile Leu Tyr
85 90 95
Phe Met Ser Thr Val His Cys Pro Ser Phe Val Met Lys Lys Thr Cys
100 105 110
Leu Arg Val Pro Leu Val Gly Tyr Ile Ala Met Glu Leu Gly Gly Val
115 120 125
Ile Val Asp Arg Glu Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg
130 135 140
Asp Arg Val Gln Glu Pro Pro Arg Asp Ser Ser Ser Glu Lys His His
145 150 155 160
Ala Gln Pro Leu Leu Val Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser
165 170 175
Cys Leu Leu Gln Phe Lys Thr Gly Ala Phe Arg Pro Gly Ala Pro Val
180 185 190
Leu Pro Val Val Leu Glu Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe
195 200 205
Ser Pro Ala Tyr Glu Ser Val His Thr Pro Ala His Leu Leu Arg Met
210 215 220
Leu Ala Gln Trp Arg His Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr
225 230 235 240
Glu Pro Ser Ala Ala Glu Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn
245 250 255
Val Arg Asp Glu Met Ala Arg Ala Leu Lys Val Pro Thr Val Glu Gln
260 265 270
Ser Tyr Arg Asp Lys Leu Val Tyr His Ala Asp Leu Met Pro His Tyr
275 280 285
Gln Lys Ala Gly Pro Gly Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu
290 295 300
Leu
305

<210> 3

<211> 1701

<212> DNA

<213> Physcomitrella patens

<220>

<221> misc_feature

<223> LPAAT

<400> 3

<210> 4

<211> 714

<212> DNA

<213> *Physcomitrella patens*

<220>

62212 CDS

<232> (1) (714)

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1400s

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Met Ala Leu Met Tyr Ile Cys Asn Leu Leu Tyr Asn Leu His Leu Phe
1 5 10 15
tct gtt gtt tct cta gca agt aat tca tat ttg ctt aat gta ctt agc 96
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser
20 25 30
aat ttg tca ttt ttg act tat tgc gat gta aat gtg att gac tae tat 144
Asn Leu Ser Phe Leu Thr Tyr Cys Asn Val Asn Val Ile Asn Tyr Tyr

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35	40	45	
gac agt gaa gcg aaa cgg gac acg ggc aat gca att gga aga gag aaa			192
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys			
50	55	60	
ggc tat ccg gag ctt gtc aat gtg ctt caa cct cgc act cgt ggc ttt			240
Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe			
65	70	75	80
gtg act tgc ctt tct caa tcc cgc tgc tct ttg gat gca gtt tat gac			288
Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp			
85	90	95	
ctc act ata ggg tac aag aag cgg tgt ccc ttg ttc atc aac aat gta			336
Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val			
100	105	110	
tcc gga acc gat cca tcc gaa gtg cac att cac att cgc cga ata cca			384
Phe Gly Thr Asp Pro Ser Glu Val His Ile Arg Arg Ile Pro			
115	120	125	
att tcc gag att cct caa tca gaa gac ggt atg acg cag tgg ctg tat			432
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr			
130	135	140	
gtt cta ttt tat caa aag gac cat agt ttg gcc agt ttt agt aag aca			480
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr			
145	150	155	160
ggt tcc ttc cct gac aat gga att gaa gag agc cct ttg aac ata gtg			528
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val			
165	170	175	
gaa ggt gtt tgc aat gtt gct cta cac gta gtc ctt agc ggt tgg gta			576
Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gln Trp Val			
180	185	190	
ttc tgg tgc ttg ttt cat tcc gtt tgg ttg aag ctt tat gtc gct ttc			624
Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe			
195	200	205	
gct agt ttg ctg ctc gcg ttt agt acc tat ttt gat tgg aga gca cct aaa			672
Ala Ser Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys			
210	215	220	
ccg gtt tac tct agt cta cgt act aaa aga aaa atc gtc taa			714
Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val			
225	230	235	

<210> 5

<211> 237

<212> PRT

<213> Physcomitrella patens

<400> 5

Met Ala Leu Met Tyr Ile Cys Asn Leu Leu Tyr Asn Leu His Leu Phe			
1	5	10	15
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser			
20	25	30	
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr			
35	40	45	
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys			
50	55	60	

Gly	Tyr	Pro	Glu	Leu	Val	Asn	Val	Leu	Gln	Pro	Arg	Thr	Arg	Gly	Phe
65				70					75						80
Val	Thr	Cys	Leu	Ser	Gln	Ser	Arg	Cys	Ser	Leu	Asp	Ala	Val	Tyr	Asp
					85				90					95	
Leu	Thr	Ile	Gly	Tyr	Lys	Lys	Arg	Cys	Pro	Leu	Phe	Ile	Asn	Asn	Val
					100				105					110	
Phe	Gly	Thr	Asp	Pro	Ser	Glu	Val	Ile	His	Ile	Arg	Arg	Ile	Pro	
					115				120					125	
Ile	Ser	Glu	Ile	Pro	Gln	Ser	Glu	Asp	Gly	Met	Thr	Gln	Trp	Leu	Tyr
					130				135					140	
Asp	Leu	Phe	Tyr	Gln	Lys	Asp	Gln	Met	Leu	Ala	Ser	Phe	Ser	Lys	Thr
145					150				155					160	
Gly	Ser	Phe	Pro	Asp	Ser	Gly	Ile	Glu	Glu	Ser	Pro	Leu	Asn	Ile	Val
					165				170					175	
Glu	Gly	Val	Cys	Asn	Val	Ala	Leu	His	Val	Val	Leu	Ser	Gly	Trp	Val
					180				185					190	
Phe	Trp	Cys	Leu	Phe	His	Ser	Val	Trp	Leu	Lys	Leu	Tyr	Val	Ala	Phe
					195				200					205	
Ala	Ser	Leu	Leu	Ala	Phe	Ser	Thr	Tyr	Phe	Asp	Trp	Arg	Pro	Lys	
					210				215					220	
Pro	Val	Tyr	Ser	Ser	Leu	Arg	Thr	Lys	Arg	Lys	Ile	Val			
					225				230					235	

<210> 6

<211> 507

<212> DNA

<213> *Physcomitrella patens*

<220>

<221> misc_feature

<223> LPAAT

<400> 6

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accggactga	tgtcactgt	aggcaccatg	cggctggcaa	cgttccggca	agggtctgtgg	120
acatatactgt	gtcccaactgt	atgttgttcc	cggaaggccac	taccaccaat	ggcagagcaa	180
taatcgccctt	caaaaacagga	gcatttccgtc	ctggtcctccc	tgtgcagccaa	atggttatata	240
gataccctca	caagtatgtc	aacccttctt	ggtgtgacca	aggaggctccg	ttggtcgttgc	300
tgttgtcaatgt	gtatgactcaat	ttccatcaacc	acatggggat	tgtatatttg	ccgggtcatqa	360
ageccaactgt	gagagatgt	aaataacccte	atgaatccgtc	aagttagatgt	ccgcagegaga	420
tggctaaatgc	gttggcgtac	aaacacactt	tctggatatt	aagctagcgc		480
tggctgcaga	aaaagctcaaa	cacgcctt				507

<210> 7

<211> 1566

<212> DNA

<213> *Physcomitrella patens*

<220>

<221> CDS

<222> (1)..(1566)

<223> LPAAT

<400> 7

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Met Glu Ser Thr Ala Asp Val Gly Met Ser Asp Asp Asp Pro Ile Leu	
1 5 10 15	
ctc aac ggg ctc gaa acg cca cta ctg gct gaa ttt cct ctt ggc gaa	96
Leu Asn Gly Leu Glu Thr Pro Leu Leu Ala Glu Phe Pro Leu Gly Glu	
20 25 30	
cgg cct aca ata ggg ccg gag gca cca gta aat ccc ttc cat gaa ccc	144
Arg Pro Thr Ile Gly Pro Glu Ala Pro Val Asn Pro Phe His Glu Pro	
35 40 45	
gat ggt ggt tgg aag acc aac aac gag tgg aat tac ttt caa atg atg	192
Asp Gly Gly Trp Lys Thr Asn Asn Glu Trp Asn Tyr Phe Gln Met Met	
50 55 60	
aaa tcc att ttg ctg att cca ctt ctt ctc gtt cgt cta gtg agc atg	240
Lys Ser Ile Leu Leu Ile Pro Leu Leu Leu Val Arg Leu Val Ser Met	
65 70 75 80	
ata aca atc gta gca ttt gga tat gtg tgg atc agg att tgt ctg atc	288
Ile Thr Ile Val Ala Phe Gly Tyr Val Trp Ile Arg Ile Cys Leu Ile	
85 90 95	
ggc gtc aca gat ccc ttg ttt aag	